SEQUENCE LISTING

(1) GENERAL INFORMATION:

   (i) APPLICANT: Conkling, Mark A.
                Mendu, Nandini
                Song, Wen

  (ii) TITLE OF INVENTION: Regulation of Quinolate Phosphoribosyl
       Transferase Expression

 (iii) NUMBER OF SEQUENCES: 4

  (iv) CORRESPONDENCE ADDRESS:
     (A) ADDRESSEE: Kenneth Sibley, Bell Seltzer Park & Gibson
     (B) STREET: Post Office Drawer 34009
     (C) CITY: Charlotte
     (D) STATE: North Carolina
     (E) COUNTRY: USA
     (F) ZIP: 28234

   (v) COMPUTER READABLE FORM:
     (A) MEDIUM TYPE: Floppy disk
     (B) COMPUTER: IBM PC compatible
     (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

  (vi) CURRENT APPLICATION DATA:
     (A) APPLICATION NUMBER:
     (B) FILING DATE:
     (C) CLASSIFICATION:

 (viii) ATTORNEY/AGENT INFORMATION:
     (A) NAME: Sibley, Kenneth D.
     (B) REGISTRATION NUMBER: 31,665
     (C) REFERENCE/DOCKET NUMBER: 5051-338P

  (ix) TELECOMMUNICATION INFORMATION:
     (A) TELEPHONE: 919-420-2200
     (B) TELEFAX: 919-881-3175

(2) INFORMATION FOR SEQ ID NO:1:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 1399 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: cDNA

  (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 52..1104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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CAAAAACTAT TTTCCACAAA ATTCATTTCA CAACCCCCCC AAAAAAAAAC C ATG TTT          57
                                                          Met Phe
                                                            1

AGA GCT ATT CCT TTC ACT GCT ACA GTG CAT CCT TAT GCA ATT ACA GCT         105
Arg Ala Ile Pro Phe Thr Ala Thr Val His Pro Tyr Ala Ile Thr Ala
          5                  10                  15

CCA AGG TTG GTG GTG AAA ATG TCA GCA ATA GCC ACC AAG AAT ACA AGA         153
Pro Arg Leu Val Val Lys Met Ser Ala Ile Ala Thr Lys Asn Thr Arg
         20                  25                  30

GTG GAG TCA TTA GAG GTG AAA CCA CCA GCA CAC CCA ACT TAT GAT TTA         201
Val Glu Ser Leu Glu Val Lys Pro Pro Ala His Pro Thr Tyr Asp Leu
 35                  40                  45                  50

AAG GAA GTT ATG AAA CTT GCA CTC TCT GAA GAT GCT GGG AAT TTA GGA         249
Lys Glu Val Met Lys Leu Ala Leu Ser Glu Asp Ala Gly Asn Leu Gly
                 55                  60                  65

GAT GTG ACT TGT AAG GCG ACA ATT CCT CTT GAT ATG GAA TCC GAT GCT         297
Asp Val Thr Cys Lys Ala Thr Ile Pro Leu Asp Met Glu Ser Asp Ala
                 70                  75                  80

CAT TTT CTA GCA AAG GAA GAC GGG ATC ATA GCA GGA ATT GCA CTT GCT         345
His Phe Leu Ala Lys Glu Asp Gly Ile Ile Ala Gly Ile Ala Leu Ala
             85                  90                  95

GAG ATG ATA TTC GCG GAA GTT GAT CCT TCA TTA AAG GTG GAG TGG TAT         393
Glu Met Ile Phe Ala Glu Val Asp Pro Ser Leu Lys Val Glu Trp Tyr
        100                 105                 110

GTA AAT GAT GGC GAT AAA GTT CAT AAA GGC TTG AAA TTT GGC AAA GTA         441
Val Asn Asp Gly Asp Lys Val His Lys Gly Leu Lys Phe Gly Lys Val
115                 120                 125                 130

CAA GGA AAC GCT TAC AAC ATT GTT ATA GCT GAG AGG GTT GTT CTC AAT         489
Gln Gly Asn Ala Tyr Asn Ile Val Ile Ala Glu Arg Val Val Leu Asn
                135                 140                 145

TTT ATG CAA AGA ATG AGT GGA ATA GCT ACA CTA ACT AAG GAA ATG GCA         537
Phe Met Gln Arg Met Ser Gly Ile Ala Thr Leu Thr Lys Glu Met Ala
                150                 155                 160

GAT GCT GCA CAC CCT GCT TAC ATC TTG GAG ACT AGG AAA ACT GCT CCT         585
Asp Ala Ala His Pro Ala Tyr Ile Leu Glu Thr Arg Lys Thr Ala Pro
            165                 170                 175
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GGA TTA CGT TTG GTG GAT AAA TGG GCG GTA TTG ATC GGT GGG GGG AAG        633
Gly Leu Arg Leu Val Asp Lys Trp Ala Val Leu Ile Gly Gly Gly Lys
    180                 185                 190

AAT CAC AGA ATG GGC TTA TTT GAT ATG GTA ATG ATA AAA GAC AAT CAC        681
Asn His Arg Met Gly Leu Phe Asp Met Val Met Ile Lys Asp Asn His
195                 200                 205                 210

ATA TCT GCT GCT GGA GGT GTC GGC AAA GCT CTA AAA TCT GTG GAT CAG        729
Ile Ser Ala Ala Gly Gly Val Gly Lys Ala Leu Lys Ser Val Asp Gln
                215                 220                 225

TAT TTG GAG CAA AAT AAA CTT CAA ATA GGG GTT GAG GTT GAA ACC AGG        777
Tyr Leu Glu Gln Asn Lys Leu Gln Ile Gly Val Glu Val Glu Thr Arg
            230                 235                 240

ACA ATT GAA GAA GTA CGT GAG GTT CTA GAC TAT GCA TCT CAA ACA AAG        825
Thr Ile Glu Glu Val Arg Glu Val Leu Asp Tyr Ala Ser Gln Thr Lys
            245                 250                 255

ACT TCG TTG ACT AGG ATA ATG CTG GAC AAT ATG GTT GTT CCA TTA TCT        873
Thr Ser Leu Thr Arg Ile Met Leu Asp Asn Met Val Val Pro Leu Ser
    260                 265                 270

AAC GGA GAT ATT GAT GTA TCC ATG CTT AAG GAG GCT GTA GAA TTG ATC        921
Asn Gly Asp Ile Asp Val Ser Met Leu Lys Glu Ala Val Glu Leu Ile
275                 280                 285                 290

AAT GGG AGG TTT GAT ACG GAG GCT TCA GGA AAT GTT ACC CTT GAA ACA        969
Asn Gly Arg Phe Asp Thr Glu Ala Ser Gly Asn Val Thr Leu Glu Thr
                295                 300                 305

GTA CAC AAG ATT GGA CAA ACT GGT GTT ACC TAC ATT TCT AGT GGT GCC        1017
Val His Lys Ile Gly Gln Thr Gly Val Thr Tyr Ile Ser Ser Gly Ala
                310                 315                 320

CTG ACG CAT TCC GTG AAA GCA CTT GAC ATT TCC CTG AAG ATC GAT ACA        1065
Leu Thr His Ser Val Lys Ala Leu Asp Ile Ser Leu Lys Ile Asp Thr
        325                 330                 335

GAG CTC GCC CTT GAA GTT GGA AGG CGT ACA AAA CGA GCA TGAGCGCCAT         1114
Glu Leu Ala Leu Glu Val Gly Arg Arg Thr Lys Arg Ala
    340                 345                 350

TACTTCTGCT ATAGGGTTGG AGTAAAAGCA GCTGAATAGC TGAAAGGTGC AAATAAGAAT     1174

CATTTTACTA GTTGTCAAAC AAAAGATCCT TCACTGTGTA ATCAAACAAA AAGATGTAAA     1234

TTGCTGGAAT ATCTCAGATG GCTCTTTTCC AACCTTATTG CTTGAGTTGG TAATTTCATT     1294

ATAGCTTTGT TTTCATGTTT CATGGAATTT GTTACAATGA AAATACTTGA TTTATAAGTT     1354

TGGTGTATGT AAAATTCTGT GTTACTTCAA ATATTTTGAG ATGTT                     1399
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(2) INFORMATION FOR SEQ ID NO:2:

      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 351 amino acids
         (B) TYPE: amino acid
         (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: protein

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Phe Arg Ala Ile Pro Phe Thr Ala Thr Val His Pro Tyr Ala Ile
 1               5                  10                  15

Thr Ala Pro Arg Leu Val Val Lys Met Ser Ala Ile Ala Thr Lys Asn
                20                  25                  30

Thr Arg Val Glu Ser Leu Glu Val Lys Pro Pro Ala His Pro Thr Tyr
          35                  40                  45

Asp Leu Lys Glu Val Met Lys Leu Ala Leu Ser Glu Asp Ala Gly Asn
    50                  55                  60

Leu Gly Asp Val Thr Cys Lys Ala Thr Ile Pro Leu Asp Met Glu Ser
 65                  70                  75                  80

Asp Ala His Phe Leu Ala Lys Glu Asp Gly Ile Ile Ala Gly Ile Ala
                85                  90                  95

Leu Ala Glu Met Ile Phe Ala Glu Val Asp Pro Ser Leu Lys Val Glu
            100                 105                 110

Trp Tyr Val Asn Asp Gly Asp Lys Val His Lys Gly Leu Lys Phe Gly
        115                 120                 125

Lys Val Gln Gly Asn Ala Tyr Asn Ile Val Ile Ala Glu Arg Val Val
    130                 135                 140

Leu Asn Phe Met Gln Arg Met Ser Gly Ile Ala Thr Leu Thr Lys Glu
145                 150                 155                 160

Met Ala Asp Ala Ala His Pro Ala Tyr Ile Leu Glu Thr Arg Lys Thr
                165                 170                 175

Ala Pro Gly Leu Arg Leu Val Asp Lys Trp Ala Val Leu Ile Gly Gly
            180                 185                 190

Gly Lys Asn His Arg Met Gly Leu Phe Asp Met Val Met Ile Lys Asp
        195                 200                 205

Asn His Ile Ser Ala Ala Gly Gly Val Gly Lys Ala Leu Lys Ser Val
    210                 215                 220

Asp Gln Tyr Leu Glu Gln Asn Lys Leu Gln Ile Gly Val Glu Val Glu
225                 230                 235                 240
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Thr Arg Thr Ile Glu Glu Val Arg Glu Val Leu Asp Tyr Ala Ser Gln
            245   250   255

Thr Lys Thr Ser Leu Thr Arg Ile Met Leu Asp Asn Met Val Val Pro
            260   265   270

Leu Ser Asn Gly Asp Ile Asp Val Ser Met Leu Lys Glu Ala Val Glu
            275   280   285

Leu Ile Asn Gly Arg Phe Asp Thr Glu Ala Ser Gly Asn Val Thr Leu
        290   295   300

Glu Thr Val His Lys Ile Gly Gln Thr Gly Val Thr Tyr Ile Ser Ser
305   310   315   320

Gly Ala Leu Thr His Ser Val Lys Ala Leu Asp Ile Ser Leu Lys Ile
            325   330   335

Asp Thr Glu Leu Ala Leu Glu Val Gly Arg Arg Thr Lys Arg Ala
            340   345   350

(2) INFORMATION FOR SEQ ID NO:3:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1053 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: cDNA

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGTTTAGAG CTATTCCTTT CACTGCTACA GTGCATCCTT ATGCAATTAC AGCTCCAAGG   60

TTGGTGGTGA AAATGTCAGC AATAGCCACC AAGAATACAA GAGTGGAGTC ATTAGAGGTG   120

AAACCACCAG CACACCCAAC TTATGATTTA AAGGAAGTTA TGAAACTTGC ACTCTCTGAA   180

GATGCTGGGA ATTTAGGAGA TGTGACTTGT AAGGCGACAA TTCCTCTTGA TATGGAATCC   240

GATGCTCATT TTCTAGCAAA GGAAGACGGG ATCATAGCAG GAATTGCACT TGCTGAGATG   300

ATATTCGCGG AAGTTGATCC TTCATTAAAG GTGGAGTGGT ATGTAAATGA TGGCGATAAA   360

GTTCATAAAG GCTTGAAATT TGGCAAAGTA CAAGGAAACG CTTACAACAT TGTTATAGCT   420

GAGAGGGTTG TTCTCAATTT TATGCAAAGA ATGAGTGGAA TAGCTACACT AACTAAGGAA   480

ATGGCAGATG CTGCACACCC TGCTTACATC TTGGAGACTA GGAAAACTGC TCCTGGATTA   540

CGTTTGGTGG ATAAATGGGC GGTATTGATC GGTGGGGGGA AGAATCACAG AATGGGCTTA   600

TTTGATATGG TAATGATAAA AGACAATCAC ATATCTGCTG CTGGAGGTGT CGGCAAAGCT   660

CTAAAATCTG TGGATCAGTA TTTGGAGCAA AATAAACTTC AAATAGGGGT TGAGGTTGAA   720

ACCAGGACAA TTGAAGAAGT ACGTGAGGTT CTAGACTATG CATCTCAAAC AAAGACTTCG   780

TTGACTAGGA TAATGCTGGA CAATATGGTT GTTCCATTAT CTAACGGAGA TATTGATGTA   840

TCCATGCTTA AGGAGGCTGT AGAATTGATC AATGGGAGGT TTGATACGGA GGCTTCAGGA   900

AATGTTACCC TTGAAACAGT ACACAAGATT GGACAAACTG GTGTTACCTA CATTTCTAGT   960

GGTGCCCTGA CGCATTCCGT GAAAGCACTT GACATTTCCC TGAAGATCGA TACAGAGCTC   1020

GCCCTTGAAG TTGGAAGGCG TACAAAACGA GCA   1053